

5' NNG CGG CCT CTG ACA CCA GCA CAG CAA ACC CGC CGG GAT CAA AGT GTA CCA GTC	9	18	27	36	45	54
X R P L T P A Q Q T R R D Q S V P V						
63 GGC AGC ATG GCT ACG AAA TGT GGG AAT TGT GGA CCC GGC TAC TCC ACC CCT CTG		72	81	90	99	108
G S M A T K C G N C G P G Y S T P L						
117 GAG GCC ATG AAA GGA CCC AGG GAA GAG ATC GTC TAC CTG CCC TGC ATT TAC CGA		126	135	144	153	162
E A M K G P R E E I V Y L P C I Y R						
171 AAC ACA GGC ACT GAG GCC CCA GAT TAT CTG GCC ACT GTG GAT GTT GAC CCC AAG		180	189	198	207	216
N T G T E A P D Y L A T V D V D P K						
225 TCT CCC CAG TAT TGC CAG GTC ATC CAC CGG CTG CCC ATG CCC AAC CTG AAG GAC		234	243	252	261	270
S P Q Y C Q V I H R L P M P N L K D						
279 GAG CTG CAT CAC TCA GGA TGG AAC ACC TGC AGC AGC TGC TTC GGT GAT AGC ACC		288	297	306	315	324
E L H H S G W N T C S S C F G D S T						
333 AAG TCG CGC ACC AAG CTG GTG CTG CCC AGT CTC ATC TCC TCT CGC ATC TAT GTG		342	351	360	369	378
K S R T K L V L P S L I S S R I Y V						

FIGURE 1A

387	GTG GAC GTG GGC TCT GAG CCC CGG GCC CCA AAG CTG CAC AAG GTC ATT GAG CCC	405	414	423	432
	V D V G S E P R A P K L H K V I E P				
441	AAG GAC ATC CAT GCC AAG TGC GAA CTG GCC TTT CTC CAC ACC AGC CAC TGC CTG	459	468	477	486
	K D I H A K A C E L A F L H T S H C L				
495	GCC AGC GGG GAA GTG ATG ATC AGC TCC CTG GGA GAC GTC AAG GGC AAT GGC AAA	513	522	531	540
	A S G E V M I S S L G D V K G N G K				
549	GGG GGT TTT GTG CTG GAT GGG GAG ACG TTC GAG GTG AAG GGG ACA TGG GAG	567	576	585	594
	G G F V L L D G E T F E V K G T W E				
603	AGA CCT GGG GGT GCT GCA CCG TTG GGC TAT GAC TTC TGG TAC CAG CCT CGA CAC	621	630	639	648
	R P G G A A P L G Y D F W Y Q P R H				
657	AAT GTC ATG ATC AGC ACT GAG TGG GCA GCT CCC AAT GTC TTA CGA GAT GGC TTC	675	684	693	702
	N V M I S T E W A A P N V L R D G F				
711	AAC CCC GCT GAT GTG GAG GCT GGA CTG TAC GGG AGC CAC TTA TAT GTA TGG GAC	729	738	747	756
	N P A D V E A G L Y G S H L Y V W D				

FIGURE 1B

765	774	783	792	801	810
TGG CAG CGC CAT GAG ATT GTG CAG ACC CTG TCT CTA AAA GAT GGG CTT ATT CCC					
W Q R H E I V Q T L S L K D G L I P					
819	828	837	846	855	864
TTG GAG ATC CGC TTC CTG CAC AAC CCA CAC GAC GCT GCC CAA GGC TTT GTG GGC TGC					
L E I R F L H N P D A A Q G F V G C					
873	882	891	900	909	918
GCA CTC AGC TCC ACC ATC CAG CGC TTC TAC AAG AAC GAG GGA GGT ACA TGG TCA					
A L S S T I Q R F Y K N E G G T W S					
927	936	945	954	963	972
GTG GAG AAG GTG ATC CAG GTG CCC CCC AAG AAA GTG AAG GGC TGG CTG CTG CCC					
V E K V I Q V P P P K K V K G W L L P					
981	990	999	1008	1017	1026
GAA ATG CCA GGC CTG ATC ACC GAC ATC CTG CTC TCC CTG GAC GAC CGC TTC CTC					
E M P G L I T D I L L S L D D R F L					
1035	1044	1053	1062	1071	1080
TAC TTC AGC AAC TGG CTG CAT GGG GAC CTG AGG CAG TAT GAC ATC TCT GAC CCA					
Y F S N W L H G D L R Q Y D I S D P					
1089	1098	1107	1116	1125	1134
CAG AGA CCC CGC CTC ACA GGA CAG CTC TTC CTC GGA GGC AGC ATT GTT AAG GGA					
Q R P R L T G Q L F L G G S I V K G					

FIGURE 1C

1143 1152 1161 1170 1179 1188  
 GGC CCT GTG CAA GTG CTG GAG GAC GAG GAA CTA AAG TCC CAG CCA GAG CCC CTA  
 G P V Q V L E D E L K S Q P E P L

1197 1206 1215 1224 1233 1242  
 GTG GTC AAG GGA AAA CGG GTG GCT GGA GGC CCT CAG ATG ATC CAG CTC AGC CTG  
 V V K G K R V A G G P Q M I Q L S L

1251 1260 1269 1278 1287 1296  
 GAT GGG AAG CGC CTC TAC ATC ACC ACG TCG CTG TAC AGT GCC TGG GAC AAG CAG  
 D G K R L Y I T T S L Y S A W D K Q

1305 1314 1323 1332 1341 1350  
 TTT TAC CCT GAT CTC ATC AGG GAA GGC TCT GTG ATG CTG CAG GTT GAT GTA GAC  
 F Y P D L I R E G S V M L Q V D V D

1359 1368 1377 1386 1395 1404  
 ACA GTA AAA GGA GGG CTG AAG TTG AAC CCC AAC TTC CTG GTG GAC TTC GGG AAG  
 T V K G G L K L N P N F L V D F G K

1413 1422 1431 1440 1449 1458  
 GAG CCC CTT GGC CCA GCC CTT GCC CAT GAG CTC CGC TAC CCT GGG GGC GAT TGT  
 E P L G P A L A H E L R Y P G G D C

1467 1476 1485 1494 1503 1512  
 AGC TCT GAC ATC TGG ATT TGA ACT CCA CCC TCA TCA CCC ACA CTC CCT ATT TTG  
 S S D I W I

FIGURE 1D

1521	1530	1539	1548	1557	1566
GGC CCT CAC TTC CTT GGG GAC CTG GCT TCA TTC TGC TCT CTC TTG GCA CCC GAC					
1575	1584	1593	1602	1611	1620
CCT TGG CAG CAT GTA CCA CAC AGC CAA GCT GAG ACT GTG GCA ATG TGT TGA GTC					
1629	1638	1647	1656	1665	1674
ATA TAC ATT TAC TGA CCA CTG TTG CTT GTT GCT CAC TGT GCT GCT TTT CCA TGA					
1683	1692	1701	1710		
GCT CTT GGA GGC ACC AAG AAA TAA ACT CGT AAC CCT GTC 3'					

FIGURE 1E

1	M	A	T	K	C	G	N	C	G	P	G	Y	S	T	P	L	E	A	M	K	G	P	R	E	E	I	V	Y	L	P	C	I	Y	R	N	T	G	T	E	A	HSEBP	
1	M	A	T	K	C	G	N	C	G	P	G	Y	S	T	P	L	E	A	M	K	G	P	R	E	E	I	V	Y	L	P	C	I	Y	R	N	T	G	T	E	A	g1374792	
1	M	A	T	K	C	T	K	C	G	P	G	Y	S	T	P	L	E	A	M	K	G	P	R	E	E	I	V	Y	L	P	C	I	Y	R	N	T	G	T	E	A	g227630	
1	M	A	T	K	C	T	K	C	G	P	G	P	S	T	P	L	E	A	M	K	G	P	R	E	E	I	V	Y	L	P	C	I	Y	R	N	T	G	T	E	A	g298710	
41	P	D	Y	L	A	T	V	D	V	D	P	K	S	P	Q	Y	C	Q	V	I	H	R	L	P	M	P	N	L	K	D	E	L	H	H	S	G	W	N	T	C	HSEBP	
41	P	D	Y	L	A	T	V	D	V	D	P	K	S	P	Q	Y	C	Q	V	I	H	R	L	P	M	P	N	L	K	D	E	L	H	H	S	G	W	N	T	Y	g1374792	
41	P	D	Y	L	A	T	V	D	V	D	P	K	S	P	Q	Y	S	Q	V	I	H	R	L	P	M	P	Y	L	K	D	E	L	H	H	S	G	W	N	T	C	g227630	
41	P	D	Y	L	A	T	V	D	V	D	P	K	S	P	Q	Y	S	Q	V	I	H	R	L	P	M	P	Y	L	K	D	E	L	H	H	S	G	W	N	T	C	g298710	
81	S	S	C	F	G	D	S	T	K	S	R	T	K	L	V	L	P	S	L	I	S	S	R	I	Y	V	V	D	V	G	S	E	P	R	A	P	K	L	H	K	HSEBP	
81	S	S	C	F	G	D	S	T	K	S	R	N	K	L	V	L	P	S	L	I	S	S	R	I	Y	V	V	D	V	G	S	E	P	G	P	Q	K	L	H	K	g1374792	
81	S	S	C	F	G	D	S	T	K	S	R	N	K	L	I	L	P	G	L	I	S	S	R	I	Y	V	V	D	V	G	S	E	P	R	A	P	K	L	H	K	g227630	
81	S	S	C	F	G	D	S	T	K	S	R	N	K	L	I	L	P	G	L	M	S	S	R	I	Y	V	V	D	V	G	S	E	P	R	A	P	K	L	H	K	g298710	
121	V	I	E	P	K	D	I	H	A	K	C	E	L	A	F	L	H	T	S	H	C	L	A	S	G	E	V	M	I	S	S	L	G	D	V	K	G	N	G	K	HSEBP	
121	V	I	E	P	K	D	I	H	A	K	C	E	L	A	C	L	H	T	S	H	C	L	A	S	G	E	V	M	I	S	S	L	G	D	V	K	G	N	G	K	g1374792	
121	V	I	E	A	S	E	I	Q	A	K	C	N	V	S	S	L	H	T	S	H	C	L	A	S	G	E	V	M	V	S	T	L	G	D	I	Q	G	N	G	K	g227630	
121	V	I	E	A	S	E	I	Q	A	K	C	N	V	S	N	T	H	T	S	H	C	L	A	S	G	E	V	M	V	S	T	L	G	D	L	Q	G	N	G	K	g298710	
161	G	G	F	V	L	L	D	G	E	T	F	F	E	V	K	G	T	W	E	R	P	G	G	A	A	P	L	G	Y	D	F	W	Y	Q	P	R	H	N	V	M	I	HSEBP
161	G	G	F	V	L	L	D	G	E	T	F	F	E	V	K	G	T	W	E	R	P	G	G	A	A	P	L	G	Y	D	F	W	Y	Q	P	R	H	N	V	M	I	g1374792
161	G	S	F	V	L	L	D	G	E	T	F	F	E	V	K	G	T	W	E	K	P	G	D	A	A	P	M	G	Y	D	F	W	Y	Q	P	R	H	N	V	M	V	g227630
161	G	S	F	V	L	L	D	G	E	T	F	F	E	V	K	G	T	W	E	K	P	G	G	A	S	P	M	G	Y	D	F	W	Y	Q	P	R	H	N	V	M	V	g298710

FIGURE 2A

201	S	T	E	W	A	A	P	N	V	L	R	D	G	F	N	P	A	D	V	E	A	G	L	Y	G	S	H	L	Y	V	W	D	W	Q	R	H	E	I	V	Q	HSEBP	g1374792	g227630	g298710
201	S	T	E	W	A	A	P	N	V	L	R	D	G	F	N	P	A	D	V	E	A	G	L	Y	G	S	H	L	Y	V	W	D	W	Q	R	H	E	I	V	Q	HSEBP	g1374792	g227630	g298710
201	S	T	E	W	A	A	P	N	V	L	R	D	G	F	N	P	A	H	V	E	A	G	L	Y	G	S	R	I	F	V	W	D	W	Q	R	H	E	I	V	Q	HSEBP	g1374792	g227630	g298710
201	S	T	E	W	A	A	P	N	V	L	R	D	G	F	N	P	A	H	V	E	A	G	L	Y	G	S	R	I	F	V	W	D	W	Q	R	H	E	I	V	Q	HSEBP	g1374792	g227630	g298710
241	T	L	S	L	K	D	G	L	I	P	L	E	I	R	F	L	H	N	P	D	A	A	Q	G	F	V	G	C	A	L	S	S	T	I	Q	R	F	Y	K	N	HSEBP	g1374792	g227630	g298710
241	T	L	S	L	K	D	G	L	I	P	L	E	I	R	F	L	H	N	P	S	A	T	Q	G	F	V	G	C	A	S	A	P	N	I	Q	R	F	Y	K	T	HSEBP	g1374792	g227630	g298710
241	T	L	Q	M	T	D	G	L	I	P	L	E	I	R	F	L	H	D	P	S	A	T	Q	G	F	V	G	C	A	S	A	P	N	I	Q	R	F	Y	K	N	HSEBP	g1374792	g227630	g298710
241	T	L	Q	M	T	D	G	L	I	P	L	E	I	R	F	L	H	D	P	S	A	T	Q	G	F	V	G	C	A	L	S	S	N	I	Q	R	F	Y	K	N	HSEBP	g1374792	g227630	g298710
281	E	G	G	T	W	S	V	E	K	V	I	Q	V	P	P	K	K	V	K	G	W	L	L	P	E	M	P	G	L	I	T	D	I	L	L	S	L	D	D	R	HSEBP	g1374792	g227630	g298710
281	R	E	G	T	W	S	V	E	K	V	I	Q	V	P	P	K	K	V	K	G	W	L	L	P	G	V	P	G	L	I	T	D	I	L	L	S	L	D	D	R	HSEBP	g1374792	g227630	g298710
281	A	E	G	T	W	S	V	E	K	V	I	Q	V	P	S	K	K	V	K	G	W	M	L	P	G	V	P	G	L	I	T	D	I	L	L	S	L	D	D	R	HSEBP	g1374792	g227630	g298710
281	G	E	G	T	W	S	V	E	K	V	I	Q	V	P	S	K	K	V	K	G	W	M	L	P	E	M	P	G	L	I	T	D	I	L	L	S	L	D	D	R	HSEBP	g1374792	g227630	g298710
321	F	L	Y	F	S	N	W	L	H	G	D	L	R	Q	Y	D	I	S	D	P	Q	R	P	R	L	T	G	Q	L	F	L	G	G	S	I	V	K	G	G	P	HSEBP	g1374792	g227630	g298710
321	F	L	Y	F	S	N	W	L	H	G	D	L	R	Q	Y	D	I	S	D	P	Q	R	P	R	L	T	G	Q	L	F	L	G	G	S	I	V	K	G	G	P	HSEBP	g1374792	g227630	g298710
321	F	L	Y	F	S	N	W	L	H	G	D	L	R	Q	Y	D	I	S	N	P	Q	K	P	R	L	A	G	Q	I	F	L	G	G	S	I	V	R	G	G	S	HSEBP	g1374792	g227630	g298710
321	F	L	Y	F	S	N	W	L	H	G	D	L	R	Q	Y	D	I	S	N	P	Q	K	P	R	L	T	G	Q	I	F	L	G	G	S	I	V	R	G	G	S	HSEBP	g1374792	g227630	g298710
361	V	Q	V	L	E	D	E	E	L	K	S	Q	P	E	P	L	V	V	K	G	K	R	V	A	G	G	P	Q	M	I	Q	L	S	L	D	G	K	R	L	Y	HSEBP	g1374792	g227630	g298710
361	V	Q	V	L	E	D	E	E	L	K	S	Q	P	E	P	L	V	V	K	G	K	R	V	A	G	G	P	Q	M	I	Q	L	S	L	D	G	K	R	L	Y	HSEBP	g1374792	g227630	g298710
361	V	Q	V	L	E	D	Q	E	L	T	C	Q	P	E	P	L	V	V	K	G	K	R	I	P	G	G	P	Q	M	I	Q	L	S	L	D	G	K	R	L	Y	HSEBP	g1374792	g227630	g298710
361	V	Q	V	L	E	D	Q	E	L	T	C	Q	P	E	P	L	V	V	K	G	K	R	I	P	G	G	P	Q	M	I	Q	L	S	L	D	G	K	R	L	Y	HSEBP	g1374792	g227630	g298710

FIGURE 2B

401	I	T	S	L	Y	S	A	W	D	K	Q	F	Y	P	D	L	I	R	E	G	S	V	M	L	Q	V	D	V	D	T	V	K	G	G	L	K	L	N	P	HSEBP
401	I	T	S	L	Y	S	A	W	E	K	Q	F	Y	P	D	L	I	R	E	G	S	V	M	L	Q	V	D	V	D	T	V	K	G	G	L	K	L	N	P	g1374792
401	A	T	S	L	Y	S	A	W	D	K	Q	F	Y	P	D	L	I	R	E	G	S	M	L	Q	I	D	V	D	T	V	N	G	G	L	K	L	N	P	g227630	
401	A	T	S	L	Y	S	A	W	D	K	Q	F	Y	P	D	L	I	R	E	G	S	V	M	L	Q	V	D	V	D	T	V	N	G	G	L	K	L	N	P	g298710

441	N	F	L	V	D	F	G	K	E	P	L	G	P	A	L	A	H	E	L	R	Y	P	G	G	D	C	S	S	D	I	W	I							HSEBP
441	N	C	L	V	D	F	G	K	E	P	L	G	P	A	L	A	H	E	L	R	Y	P	G	G	D	C	S	S	D	I	W	I							g1374792
441	N	F	L	V	D	F	G	K	L	P	L	G	A	L	A	H	E	L	R	Y	P	G	G	D	C	S	S	D	I	W	I								g227630
441	N	F	L	V	D	F	G	K	E	P	L	G	P	A	L	A	H	E	L	R	Y	P	G	G	D	C	S	S	D	I	W	I							g298710

FIGURE 2C

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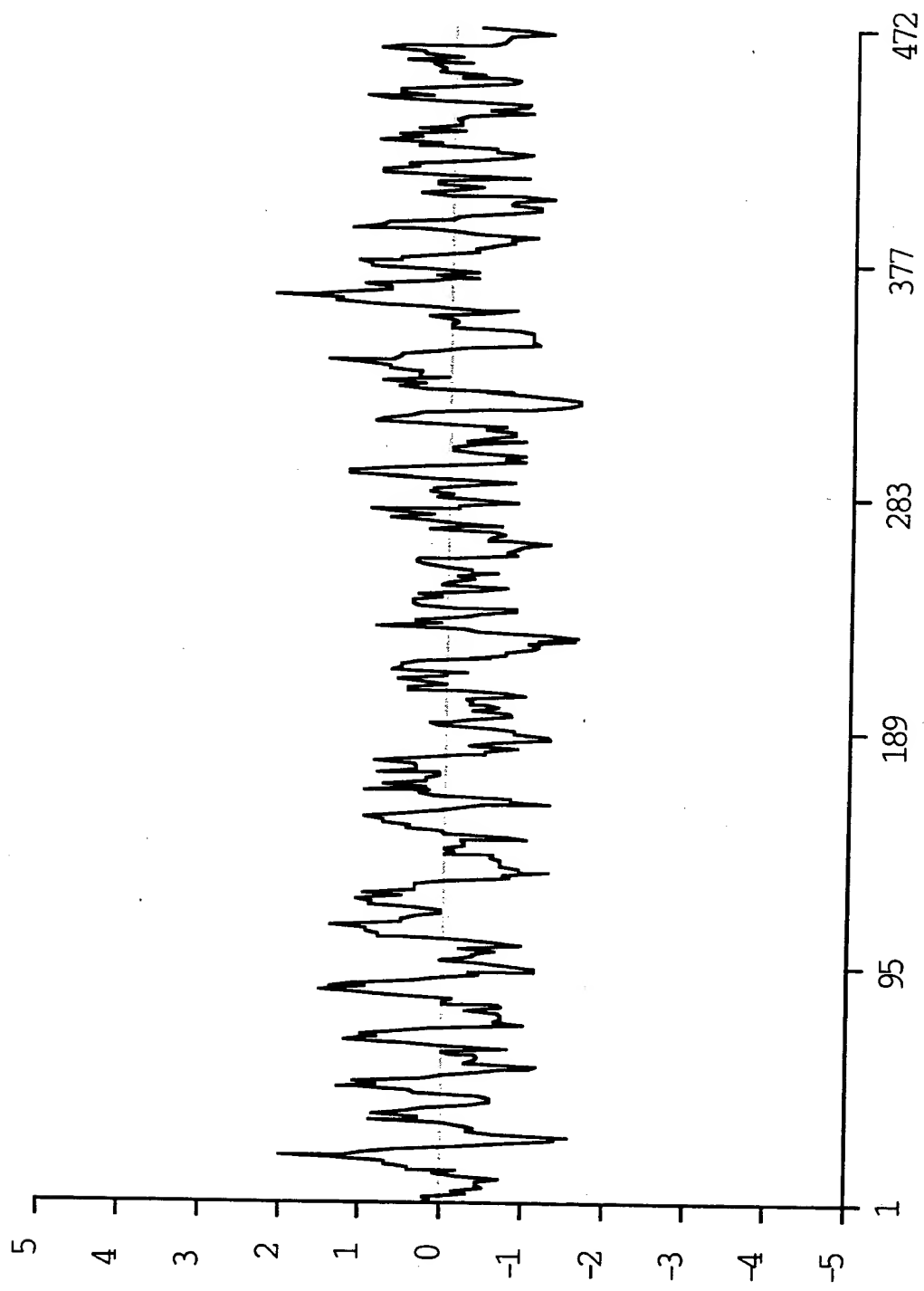


FIGURE 3

9910

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FIGURE 4

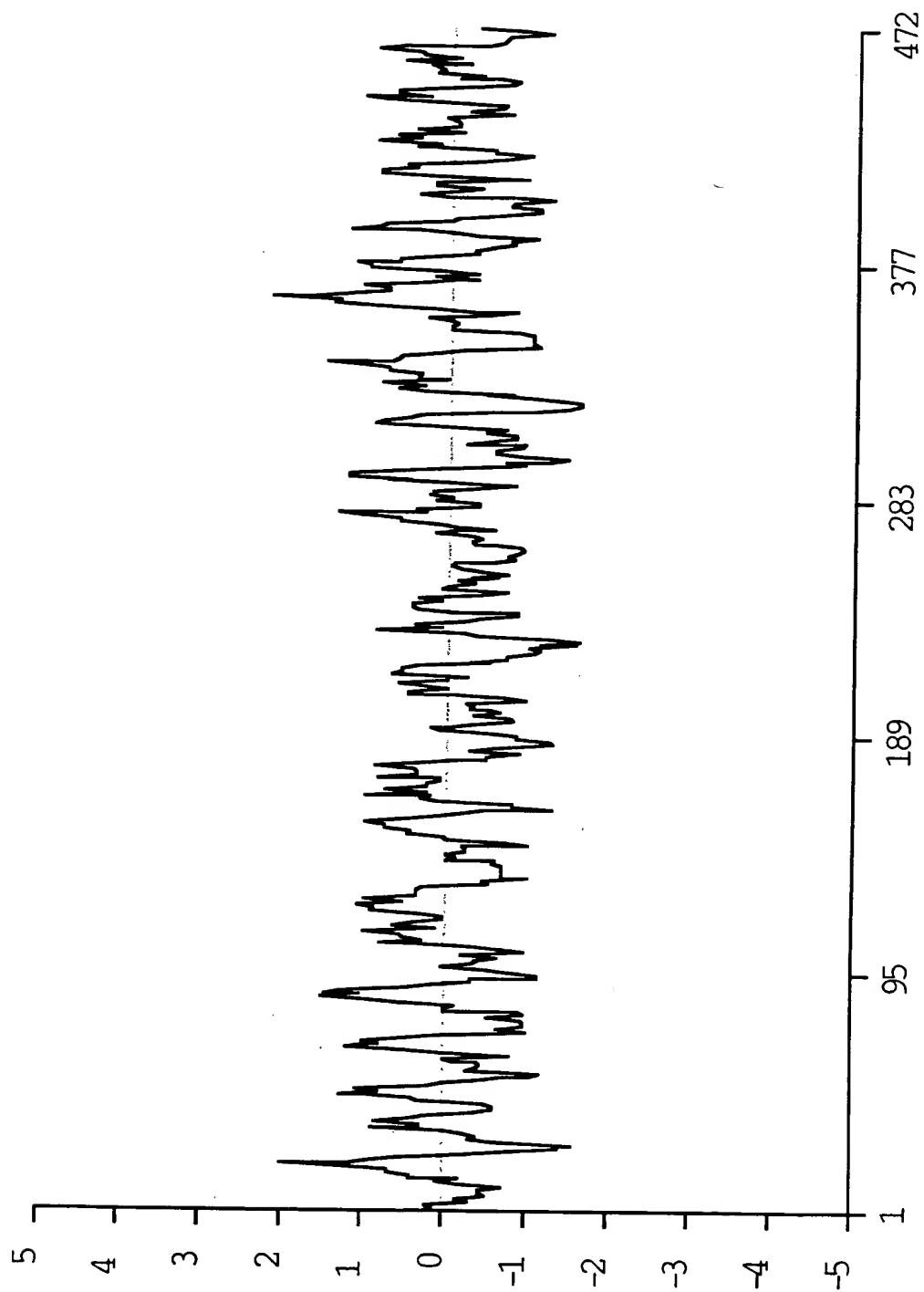


FIGURE 4

Library	Lib Description	Abun	Pct Abun
COLNNOT13	colon, ascending, 28 M	2	0.0621
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	2	0.0619
COLNNOT16	colon, 62 M, match to COLNTUT03	2	0.0589
COLNNOT11	colon, 60 M	1	0.0307
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
PANCTUT01	pancreatic tumor, 65 F, match to PANCNOT08	1	0.0257
COLNTUT02	colon tumor, 75 match to COLNNOT01	1	0.0220
LUNGNOT03	lung, 79 M, match to LUNGUT02	1	0.0200
LUNGUT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	1	0.0188
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0163
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0152
LUNGAST01	lung, asthma, 17 M	1	0.0150
THYRNOT03	thyroid tumor, adenoma, 28 F	1	0.0138

FIGURE 5